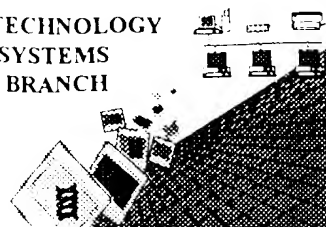


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/925,055 B

Source: 1644

Date Processed by STIC: 2/19/2002

217
1651
RECEIVED
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TECH CENTER 1600-2300

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/925,055B
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) <u>30</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



1644

RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/09/925,055B

TIME: 12:20:18

Input Set : A:\00-56 SEQ.txt

Output Set: N:\CRF3\02192002\I925055B.raw

Does it compile
correctly? (yes/no)

3 <110> APPLICANT: Kindsvogel, Wayne R.
 4 Topouzis, Stavros
 6 <120> TITLE OF INVENTION: SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS
 8 <130> FILE REFERENCE: 00-56
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/925,055B
 C--> 10 <141> CURRENT FILING DATE: 2001-08-08
 10 <150> PRIOR APPLICATION NUMBER: US 60/223,827
 11 <151> PRIOR FILING DATE: 2000-08-08
 13 <150> PRIOR APPLICATION NUMBER: US 60/250,876
 14 <151> PRIOR FILING DATE: 2000-12-01
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 18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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 22 <212> TYPE: DNA
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 32 1 5
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 35 Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
 36 10 15 20
 38 ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150
 39 Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
 40 25 30 35
 42 acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
 43 Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
 44 40 45 50 55
 46 gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246
 47 Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
 48 60 65 70
 50 cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac 294
 51 Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
 52 75 80 85
 54 ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc 342
 55 Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly
 56 90 95 100
 58 cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act 390
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RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/09/925,055B

TIME: 12:20:18

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Output Set: N:\CRF3\02192002\I925055B.raw

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64	120 125 130 135			
66	cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc	486		
67	Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly			
68	140 145 150			
70	cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta	534		
71	His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu			
72	155 160 165			
74	gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag	582		
75	Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln			
76	170 175 180			
78	aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc	630		
79	Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly			
80	185 190 195			
82	acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac	678		
83	Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr			
84	200 205 210 215			
86	atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc	726		
87	Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe			
88	220 225 230			
90	tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc	774		
91	Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys			
92	235 240 245			
94	tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822		
95	Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser			
96	250 255 260			
98	ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870		
99	Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln			
100	265 270 275			
102	gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918		
103	Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu			
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111	Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu			
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114	ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc	1062		
115	Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro			
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118	cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc	1110		
119	Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val			
120	345 350 355			
122	ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca	1158		
123	Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro			
124	360 365 370 375			

RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/09/925,055B

TIME: 12:20:18

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Output Set: N:\CRF3\02192002\I925055B.raw

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130   cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg      1254
131   Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met
132               395                      400                      405
134   gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa      1302
135   Glu Gly Ser Gly Lys Asp Ser Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
136               410                      415                      420
138   cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc      1350
139   His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
140               425                      430                      435
142   tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg      1398
143   Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
144   440                      445                      450                      455
146   gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc      1446
147   Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
148               460                      465                      470
150   aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg      1494
151   Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
152               475                      480                      485
154   aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag      1542
155   Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
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158   atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca      1590
159   Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
160   505                      510                      515
162   tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc      1638
163   Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
164   520                      525                      530                      535
166   ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca      1686
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170   gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc      1734
173   Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
174               555                      560                      565
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177   Leu Thr Val Gln Trp Glu Ser
178               570
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182   ggcccctgcc atgggtgcgc tcctcaccgg aacaaagcag catgataagg actgcagcgg      1965
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184   aaatgacagt gcaaggagga aatgcaggga aactcccag gtccagagcc ccacctccta      2085
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187   gaagagagcc tggaaaagaa ccaggcctgg aaaagaacca gaaggaggct gggcagaacc      2265
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RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/09/925,055B

TIME: 12:20:18

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192 gctgtggccc ctggacgggt acaataacac actgtactga tgtcacaact ttgcaagctc 2565
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195 ataacaccta cctcatggag ttgtggtgaa gatgaaatga agtcatgtct ttaaagtgtc 2745
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197 aaaaaaaaaa atagcggccg cctcga 2831

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200 <211> LENGTH: 574

201 <212> TYPE: PRT

202 <213> ORGANISM: Homo sapien

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208 20 25 30
209 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
210 35 40 45
211 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
212 50 55 60
213 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
214 65 70 75 80
215 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
216 85 90 95
217 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
218 100 105 110
219 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
220 115 120 125
221 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
222 130 135 140
223 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
224 145 150 155 160
225 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
226 165 170 175
227 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
228 180 185 190
229 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
230 195 200 205
231 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
232 210 215 220
233 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
234 225 230 235 240
235 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
236 245 250 255
237 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
238 260 265 270
239 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
240 275 280 285

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RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/09/925,055B

TIME: 12:20:18

Input Set : A:\00-56 SEQ.txt

Output Set: N:\CRF3\02192002\I925055B.raw

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243 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
244      305      310      315      320
245 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
246      325      330      335
247 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
248      340      345      350
249 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
250      355      360      365
251 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
252      370      375      380
253 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
254      385      390      395      400
255 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
256      405      410      415
259 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
260      420      425      430
261 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
262      435      440      445
263 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
264      450      455      460
265 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
266      465      470      475      480
267 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
268      485      490      495
269 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
270      500      505      510
271 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
272      515      520      525
273 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
274      530      535      540
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281 <211> LENGTH: 211
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289      20      25      30
290 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
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09/925,055B 6

<210> SEQ ID NO 30

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<212> TYPE: PRT

<213> ORGANISM Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: :

<400> SEQUENCE: 30

*see item 11 on Encl Summary
Sheet*

VERIFICATION SUMMARY

DATE: 02/19/2002

PATENT APPLICATION: US/09/925,055B

TIME: 12:20:19

Input Set : A:\00-56 SEQ.txt

Output Set: N:\CRF3\02192002\I925055B.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1092 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:1092 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: